

Delaval, Jan

From: Jamroz, Margaret
Sent: Monday, March 25, 2002 8:29 AM
To: Delaval, Jan
Subject: 09/628,126

Jan,

Please do open search of SEQ ID NO: 23 with interference of 09/628,126.

Thanks,

Megan Jamroz

USPTO

AU 1644

Mailbox 9E12

CM1 9D04

(703) 308-8365

Margaret.Jamroz@USPTO.gov

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
ian.delaval@uspto.gov

Access DB# 63018

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
 Reference Librarian
 Biotechnology & Chemical Library
 CM1 1E07 - 703-308-4498
 jan.delaval@uspto.gov

STAFF USE ONLY

Searcher: Jan
 Searcher Phone #: 6448
 Searcher Location: _____
 Date Searcher Picked Up: 3/25/02
 Date Completed: 3/25/02
 Searcher Prep & Review Time: _____
 Clerical Prep Time: 10
 Online Time: 10

Type of Search

NA Sequence (#) _____
 AA Sequence (#) ☒ _____
 Structure (#) _____
 Bibliographic _____
 Litigation _____
 Fulltext _____
 Patent Family _____
 Other _____

Vendors and cost where applicable

STN _____
 Dialog _____
 Questel/Orbit _____
 Dr.Link _____
 Lexis/Nexis _____
 Sequence Systems ☒ _____
 WWW/Internet _____
 Other (specify) _____

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 25, 2002, 08:35:55 ; Search time 18.44 Seconds

(without alignments)

889.152 Million cell updates/sec

Title: US-09-628-126-23

Perfect score: 1118

Sequence: 1 MHVPAGSVASHLGTTSRSYF.....DTSTFPLENVLISFLYSNSD 215

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_68.*

2: PIR1.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1118	100.0	234	2 A40710	CD30 ligand - huma
2	814.5	72.9	239	2 B40710	CD30 ligand - mous
3	112	10.0	279	2 A53062	Fas ligand - mouse
4	96.5	8.6	234	1 J01344	tumor necrosis fac
5	94	8.4	235	2 I34490	tumor necrosis fac
6	93.5	8.4	547	2 T30704	rifampicin resista
7	90.5	8.1	281	2 I38707	Fas ligand - human
8	90	8.1	233	1 S22052	tumor necrosis fac
9	89	8.0	809	2 T38051	hypothetical prote
10	87.5	7.8	813	2 T12506	hypothetical prote
11	86	7.7	278	2 A49286	fas ligand - rat
12	85.5	7.6	309	2 I53384	4-1BB ligand - mou
13	85	7.6	235	1 QWMSN	tumor necrosis fac
14	84.5	7.6	232	1 S12606	tumor necrosis fac
15	83.5	7.5	234	1 JH0529	tumor necrosis fac
16	83	7.4	636	2 S70877	hypothetical prote
17	83	7.4	1385	2 T18213	paraspinal crystal
18	82	7.3	513	2 B96524	hypothetical prote
19	82	7.3	1339	2 G84764	hypothetical prote
20	81.5	7.3	461	2 JN0129	ID-myo-inositol-tr
21	81	7.2	233	1 QWHUN	tumor necrosis fac
22	81	7.2	547	2 H65107	hypothetical 61.6
23	81	7.2	1289	2 T18212	paraspinal crystal
24	80.5	7.2	430	2 T28318	ORF MSV157 hypothe
25	80.5	7.2	434	1 S61999	hypothetical prote
26	80.5	7.2	499	2 A55346	phosphoprotein pho
27	80	7.2	235	2 J00029	tumor necrosis fac
28	79.5	7.1	233	1 S24642	tumor necrosis fac
29	79	7.1	800	2 S53079	PET111 protein - y

30 78.5 7.0 426 2 S64748
31 78.5 7.0 1130 2 T29089
32 78.5 7.0 1830 2 E82909
33 77.5 6.9 492 2 S42735
34 77.5 6.9 610 2 S71758
35 77.5 6.9 623 2 B96681
36 77 6.9 329 2 T28412
37 77 6.9 456 2 B96688
38 76.5 6.8 478 2 T27714
39 76.5 6.8 619 2 S54636
40 76.5 6.8 3512 2 T17121
41 76 6.8 467 2 D86485
42 76 6.8 479 2 E42508
43 76 6.8 607 2 E70165
44 76 6.8 829 2 S72366
45 75.5 6.8 284 2 F81431

ALIGNMENTS

RESULT 1

A40710

CD30 ligand - human

C:Species: Homo sapiens (man)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000

C:Accession: A40710

R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland,

Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Girdwin, R.G.; Armitage,

Cell 73, 1349-1360, 1993

A>Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de

A:Reference number: A40710; MUID:93313964

A:Accession: A40710

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-234 <SMI>

A:Cross-references: GB:109753; NID:g349277; PIDN:AAA74594.1; P:..f349278

C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match 100.0%; Score 1118; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 2.4e-98;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHVPAGSVASHLGTTSRSYFYLTTATLALCLVFTVATIMVLVQRTDSIPK...DNVPLKG 60

Db 20 MHVPAGSVASHLGTTSRSYFYLTTATLALCLVFTVATIMVLVQRTDSIPK...NVPLKG 79

QY 61 GNCSEDLCLIKRAPFKSWAYLQVAKHLNKTLSWNRKDGILHGVRYQDC...TQFPGLY 120

Db 80 GNCSEDLCLIKRAPFKSWAYLQVAKHLNKTLSWNRKDGILHGVRYQDC...TQFPGLY 139

QY 121 FITCOLFVOCNPNVDLKLLELHINKHKKOALVTVCESGMOTKHVYQNLSCFEDYLO 180

Db 140 FITCOLFVOCNPNVDLKLLELHINKHKKOALVTVCESGMOTKHVYQNLSCFEDYLO 199

QY 181 VNTTISVNDVTFQYIDTSTFPLENVLISFLYSNSD 215

Db 200 VNTTISVNDVTFQYIDTSTFPLENVLISFLYSNSD 234

RESULT 2

B40710

CD30 ligand - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999

C:Accession: B40710

R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland,

Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Girdwin, R.G.; Armitage,

Cell 73, 1349-1360, 1993

A>Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de

A:Reference number: A40710; MUID:93313964

A:Accession: B40710

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-239 <SMI>
A:Cross-references: GB:L09754; NID:g349288; PIDN:AAA74595.1; PID:g349289
C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match 72.9%; Score 814.5; DB 2; Length 239;
Best Local Similarity 70.6%; Pred. No. 1.2e-69;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

QY 1 MHVPAGSVAS-----HLGTSRSYFVLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54
Db 20 MQVPGSVASPMWTRPWRSTSYFVLTAL-VCLVAVAILVLVQKKDSTPNTE 78

QY 55 NVPLKGCNCSEDLCLIKRAPFKSWAYLOVAKHLNKTLSWNRKDGILHGVRVODGNLVI 114
79 KAPLKGNCSEDLFCILKSTPSKSWAYLOVAKHLNKTLSWNRKDGILHGVRVODGNLVI 138
115 QPGLYFIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMQTKHYVONLSQF 174
Db 139 QPGLYFIICQLQFLVQCSNHSVDLTQLLLINSKIKKQALVTVCESGMQTKHYVONLSQF 198

QY 175 LLDYLVQNTTISVNVDTFQIDRSTPLENVLSIFLYNSD 215

Db 199 LLHYLVQNTTISVNVDTFQIDRSTPLENVLSIFLYNSD 239

RESULT 3
A53062
fas ligand - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: A53062
R:Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nagai, Y.; et al.
Cell 76, 969-976, 1994
A:Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in the fas ligand gene.
A:Reference number: A53062; MUID:94185175
A:Accession: A53062
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-279 <AK>
A:Cross-references: GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565

Query Match 10.0%; Score 112; DB 2; Length 279;
Best Local Similarity 22.6%; Pred. No. 0.0043;
Matches 38; Conservative 30; Mismatches 58; Indels 42; Gaps 6;

QY 33 FTVATIMVLVQRTDSIPNSPDVPLKGGNCSEDLCLIKRAPFKSWAYLOVAKHLNKT 92
Db 115 FTNQLKVSFFKQIANPSPSE-----KKEP-RSVAHLTGPHRSRI 156

QY 93 KLSWNR---DGLIHGVRVODGNLVIQFPGLYFIICQLQFLVQ-CPNNSVDLKLLELLINKH 148
Db 157 PLEWEDTYGTALISGVYKRGGLVINETGLYFVYSYFGRGSCNNQPLNHHKVMRNSKY 216

QY 149 ----LKKQALVTVCESGM-----QTKHYVONLSQFLL 176

Db 217 PEDLVLMEEKRLNYCTGTQIAHSSYLGAVFNLTSAHDHLYVNISQSL 264

RESULT 4
JQ1344
tumor necrosis factor alpha precursor - horse
N:Alternate names: cachectin; TNF alpha
C:Species: Equus caballus (domestic horse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: JQ1344
R:Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis factor.
A:Reference number: JQ1344; MUID:92084125

A:Accession: JQ1344
A:Molecule type: DNA
A:Residues: 1-234 <SDX>

A:Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245
C:Comment: This protein is an important proximal mediator of endotoxemia.

C:Genetics:

A:Gene: TNF-alpha

A:Introns: 62/3; 79/1; 95/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage;

F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:146-178/Disulfide bonds: #status predicted

Query Match 8.6%; Score 96.5; DB 1; Length 334;
Best Local Similarity 24.7%; Pred. No. 0.1;
Matches 48; Conservative 33; Mismatches 88; Indels 25; Gaps 8;

QY 18 SYFVLTATLALCLVFTVATIMVLVQRTDSIPNSPDVPLKGGNCSEDLCLIKRAPFK 77

Db 37 SFLLVAGATTFLCLLH---FGVIGPQREQLPNAFQSI-----NPLAOT--SSTPSD 87

QY 78 KSWAYLOVAKHLNKTLSW---NKDGIL-HGVRVODGNLVIQFPGLYFIICQLQFLVQ-C 132

Db 88 KPAHV-VANPQAEQQLWLSGRANALLANGVKLTQNLQVLVPLDGLYLIYSQVLFKGGC 146

QY 133 PNNVDL--KLELLINKHKKQALVTVCESGMQ-----KHVYONLS--LIDYLVQVN 182

Db 147 PSTHVLLTHTLSRLAVSYPSKVNLLSIAKSPCHTESPEQAEAKPWYPIYL-ICVFOLEKG 206

QY 183 TTISVNVDTFOYID 196

Db 207 DQLSAEINQPNYLD 220

RESULT 5

I54490

tumor necrosis factor alpha precursor - white-footed mouse

C:Species: Peromyscus leucopus (white-footed mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000

C:Accession: I54490

R:Crew, M.D.; Filipowsky, M.E.

Immunogenetics 35, 351-353, 1992

A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus

A:Reference number: I54490; MUID:92218012

A:Accession: I54490

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-235 <RES>

A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C:Genetics:

A:Gene: TNF

A:Introns: 62/3; 81/1; 97/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 8.4%; Score 94; DB 2; Length 235;
Best Local Similarity 24.0%; Pred. No. 0.18;
Matches 48; Conservative 31; Mismatches 85; Indels 36; Gaps 8;

QY 18 SYFVLTATLALCLVFTVATIMVLVQRTDSIPNSPDVPLKGGNCSEDLCLIKRAPFK 77

Db 37 SFLLVAGATTFLCLLH---NFGVIGPQREKFPN---NLPIIGSQAQTLTLPSS-SONSSD 89

QY 78 KSWAYLOVAKHLNKTLSWNRKDG-----ILHGVRVODGNLVIQFPGLYFIICQLQFLVQ-C 132

Db 90 KPAHV-VANHQVDEQLEWLSRGANALLANGMDLKNQVLTPADGLYLVY--LFFKGGC 148

```
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 234 AA; 26017 MW; C653615682305BIB CRC64;

Query Match
Best Local Similarity 100.0%; Score 1118; DB 1; Length 234;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHVPAGSVASHLGTSTRSYFLTTATLALCLVFTVATIMVLVQVTSIPNSPNVPLKG 60
    |||||F|||||
DQ 20 MHVPAGSVASHLGTSTRSYFLTTATLALCLVFTVATIMVLVQVTSIPNSPNVPLKG 79
    |||||F|||||

QY 61 GNCSEDLCLIKRAPFKSWAYLOVAKHLNKTLSWKNKDGILHGVRYODGNLVTOFPGLY 120
    |||||F|||||
DQ 80 GNCSEDLCLIKRAPFKSWAYLOVAKHLNKTLSWKNKDGILHGVRYODGNLVTOFPGLY 139
    |||||F|||||

QY 121 FIICOLFVQCPNNSVDLKLLELINKHKKQALVTVCSGMOTKHVYQNLQSFLDYLO 180
    |||||F|||||
DQ 140 FIICOLFVQCPNNSVDLKLLELINKHKKQALVTVCSGMOTKHVYQNLQSFLDYLO 199
    |||||F|||||

QY 181 VNTTISVNVDTFOYIDTSTFPLENLSIFLYSNSD 215
    |||||F|||||
DQ 200 VNTTISVNVDTFOYIDTSTFPLENLSIFLYSNSD 234
    |||||F|||||

RESULT 2
TNF8_MOUSE
ID TNF8_MOUSE STANDARD; PRT; 239 AA.
AC P32972;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD30 LIGAND (CD30-L).
GN TNFSF8 OR CD30LG OR CD30L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93313964; PubMed=8391931;
RA Smith C.A., Guess H.-J., Davis T., Anderson D., Farrah T.,
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAlister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RT "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
RT TNF.";
RL Cell 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L09754; AAA74595.1;
CC PIR; B40710; B40710.
CC MG; MG8328; TNFSF8.
CC InterPro; IPR003638; TNF_8.
CC InterPro; IPR000478; TNF_family.
CC Pfam; PF00229; TNF_1.
CC ProDom; PD023087; TNF_8; 1.
CC SMART; SK00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
```

```
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 44 67 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 68 239 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 239 AA; 26519 MW; 29003157DD425159 CRC64;

Query Match
Best Local Similarity 72.9%; Score 814.5; DB 1; Length 239;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

QY 1 MHVPAGSVAS-----HLGTTSTRSYFLTTATLALCLVFTVATIMVLVQVTSIPNSD 54
    |||||F|||||
DQ 20 MHVPAGSVASVWRSTPWRSTPWRSTPWRSTPWRSTPWRSTPWRSTPWRSTPWRSTP 78
    |||||F|||||

QY 55 NVPLKGGNCSEDLCLIKRAPFKSWAYLOVAKHLNKTLSWKNKDGILHGVRYODGNLV 114
    |||||F|||||
DQ 79 KAPLGGNCSEDLCLIKRAPFKSWAYLOVAKHLNKTLSWKNKDGILHGVRYODGNLV 138
    |||||F|||||

QY 115 QPGLYFIICOLFVQCPNNSVDLKLLELINKHKKQALVTVCSGMOTKHVYQNLQSOF 174
    |||||F|||||
DQ 139 QPGLYFIICOLFVQCPNNSVDLKLLELINKHKKQALVTVCSGMOTKHVYQNLQSOF 198
    |||||F|||||

QY 175 LLDYLVQVNTTISVNVDTFOYIDTSTFPLENLSIFLYSNSD 215
    |||||F|||||
DQ 199 LLDYLVQVNTTISVNVDTFOYIDTSTFPLENLSIFLYSNSD 239
    |||||F|||||

RESULT 3
FASL_MOUSE
ID FASL_MOUSE STANDARD; PRT; 279 AA.
AC P41047; O61217; Q9R1F2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FAS ANTIGEN LIGAND.
GN TNFSF6 OR APTLGI OR FASL OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RC MEDLINE=94181575; PubMed=7511063;
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand.";
RL Cell 76:969-976(1994).
CC [2]
CC SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELLING.
CC STRAIN=C57BL/6;
CC MEDLINE=95388076; PubMed=7544870;
CC Peitsch M.J., Tschopp J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family.";
RL Mol. Immunol. 32:761-772(1995).
CC [3]
CC SEQUENCE FROM N.A. (ISOFORM FASL).
CC MEDLINE=95196085; PubMed=7889405;
CC Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
CC Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster.";
RL Immunity 1:131-136(1994).
CC [4]
```

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	1118	100.0	234	1	TNF8_HUMAN	P32971 homo sapien
2	814.5	72.9	239	1	TNF8_MOUSE	P32972 mus musculus
3	112	10.0	279	1	FASL_MOUSE	P41047 mus musculus
4	96.5	8.6	234	1	TNFA_HORSE	P29553 equus caball
5	94	8.4	233	1	TNFA_MACMU	P48094 macaca mula
6	94	8.4	235	1	TNFA_PERLE	P36939 peromyscus
7	92	8.2	233	1	TNFA_MACFA	P79337 macaca fasc
8	90.5	8.1	281	1	FASL_HUMAN	P48023 homo sapien
9	90	8.1	233	1	TNFA_PAPHU	O77510 papio hamad
10	90	8.1	233	1	TNFA_PAPSP	P33620 papio sp. (
11	89	8.0	809	1	YATA_SCHPO	Q10155 schizosacch
12	86	7.7	278	1	FASL_RAT	P36940 rattus norv
13	85.5	7.6	309	1	I1BL_MOUSE	P41274 mus musculus
14	85	7.6	233	1	TNFA_CANFA	P51742 canis famil
15	85	7.6	235	1	TNFA_MOUSE	P06804 mus musculus
16	85	7.6	1220	1	CSAC_BACTU	P56955 bacillus th
17	84.5	7.6	232	1	TNFA_PIG	P23563 sus scrofa
18	83.5	7.5	234	1	TNFA_SHEEP	P23383 ovis aries
19	83	7.4	1385	1	CSAA_BACUD	Q45760 bacillus th
20	81.5	7.3	461	1	IP3K_HUMAN	P23677 homo sapien
21	81	7.2	233	1	TNFA_HUMAN	P01375 homo sapien
22	81	7.2	233	1	TNFA_MARMO	O35734 marmota mon
23	81	7.2	541	1	YHXB_ECOLI	P42640 escherichia
24	81	7.2	1289	1	CSAB_BACUD	Q45753 bacillus th
25	80.5	7.2	499	1	PPPS_RAT	P53042 rattus norv
26	80	7.2	229	1	TNFA_CEREL	P51743 cervus elap
27	80	7.2	235	1	TNFA_RAT	P16599 rattus norv
28	79.5	7.1	233	1	TNFA_BOVIN	Q06599 bos taurus
29	79	7.1	800	1	PT1L_YEAST	P08468 saccharomyc
30	78.5	7.0	234	1	TNFA_CAVPO	P51435 cavia porce
31	78.5	7.0	426	1	MMML_YEAST	P41800 saccharomyc
32	77.5	6.9	670	1	DD18_HUMAN	Q9nvp1 homo sapien
33	76	6.8	479	1	PAP1_VACCC	P21079 vaccinia vi

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 25, 2002, 08:36:50 ; Search time 22.63 Seconds
(without alignments)
1389.684 Million cell updates/sec

Title: US-09-628-126-23
Perfect score: 1118
Sequence: 1 MHVPAGSVASHLGTTSRSYF.....DTSTPFLNLSIFLYNSD 215

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_invertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Alt No.	Score	Match	Query Length	DB ID	Description
1	1094	97.9	234	4	O43404
2	100	8.9	169	11	Q9WV90
3	96.5	8.6	215	6	Q9BEE8
4	95.5	8.5	280	6	Q9BDN1
5	94.5	8.5	234	6	Q9TTJ3
6	93.5	8.4	547	12	Q98269
7	93	8.3	217	11	Q9ERG6
8	92	8.2	280	6	Q9MYL6
9	92	8.2	280	6	Q9BDM5
10	89.5	8.0	896	10	Q9W9B0
11	88.5	7.9	217	6	Q9BEG1
12	88	7.9	1109	5	Q9GTH7
13	87.5	7.8	216	6	Q9BEC4
14	87.5	7.8	813	4	Q9Y4N0
15	87.5	7.8	1003	4	Q9P207
16	85.5	7.6	462	2	Q9CM44
17	85	7.6	282	6	Q9BEA8
18	85	7.6	761	3	Q9UWJ1
19	84.5	7.6	232	4	Q9UIV3

20	83.5	7.5	431	10	O9LIF0
21	83.5	7.5	506	10	O9C5J4
22	83	7.4	372	12	O967I7
23	83	7.4	586	11	O9CRS2
24	83	7.4	636	2	O56619
25	83	7.4	636	2	O34235
26	83	7.4	636	2	O87139
27	83	7.4	640	8	O9GEV6
28	82.5	7.4	225	13	O9IB42
29	82.5	7.4	232	11	O35853
30	82.5	7.4	234	6	O28320
31	82	7.3	513	10	O9SX72
32	82	7.3	1339	10	O82180
33	81	7.2	255	2	O9QX6
34	80.5	7.2	430	12	O9YVY5
35	80.5	7.2	434	3	O02933
36	80.5	7.2	479	11	O64538
37	80.5	7.2	499	11	O35299
38	80	7.2	157	4	O43647
39	79.5	7.1	93	6	O9TTJ2
40	79.5	7.1	676	8	O9TL41
41	79	7.1	914	10	O96301
42	78.5	7.0	505	5	O9NGC2
43	78.5	7.0	660	11	O9D2E0
44	78.5	7.0	820	10	O9LLN5
45	78.5	7.0	1130	5	O18497

ALIGNMENTS

RESULT 1

O43404 ID O43404 PRELIMINARY; PRT; 234 AA.
AC O43404;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CD30L PROTEIN.
OS CD30L.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98007874; PubMed=9349718;
RA Croager E.J., Abraham L.J.;
RT "Characterisation of the human CD30 ligand gene structure".
RL Biochim. Biophys. Acta 1353:231-235(1997).
DR EMBL; AF006384; AAB97877.1;
DR EMBL; AF006381; AAB97877.1; JOINED.
DR EMBL; AF006382; AAB97877.1; JOINED.
DR EMBL; AF006383; AAB97877.1; JOINED.
DR InterPro; IPR000478; TNF_family.
DR InterPro; IPR003638; TNF_8.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD023087; TNF_8; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
DR SMART; SM00207; TNF; 1.
SQ SEQUENCE 234 AA; 25963 MW; 37BA5733C7911751 CRC64;

Query Match 97.9%; Score 1094; DB 4; Length 234;
Best Local Similarity 98.1%; Pred. No. 1.4e-101;
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSTAYPLKG 60
Db 20 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSTAYPLKG 79
Qy 61 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWNKDGILHGVRQDGNLVIQFPGLY 120

Db 80 GNCSEDLICILKRAPFKSWAYLQVAKHLNKTLSWKNKGILHGVRYQDGNLVQFPGLY 139

QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKKQALVTVCSGMOVKHYVQNLQFLDYLO 180

Db 140 FIICQLQFLVQCPNNSVDLKLLELLINKHKKKQALVTVCSGMOVKHYVQNLQFLDYLO 199

QY 181 VNTTISVNVDTFQYIDTSTFPLENVLISFLYSNSD 215

Db 200 VNTTISVNVDTFQYIDTSTFPLENVLISFLYSNSD 234

RESULT 2

Q9WV90 PRELIMINARY; PRT; 169 AA.

AC Q9WV90;

DT 01-NOV-1999 (Tremblrel. 12, Created)

RT 01-JUN-2001 (Tremblrel. 12, Last sequence update)

DE FAS LIGAND (FRAGMENT).

OS Marmota monax (Woodchuck).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sclurinae;

OC Marmota.

OX NCBI_TaxID=9995;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=HEALTHY LIVER;

RA Hodgson P.D., Grant M.D., Michalak T.I.;

RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and chronic woodchuck viral hepatitis";

RL Clin. Exp. Immunol. 0:0-0(1999).

DR EMBL; AF152368; AAD38387.1; -

DR InterPro; IPR000478; TNF_family.

DR InterPro; IPR003263; TNF_5.

DR Pfam; PF00229; TNF; 1.

DR ProDom; PD008600; TNF_5; 1.

DR ProSITE; PS00251; TNF_1; 1.

DR ProSITE; PS00049; TNF_2; 1.

DR SMART; SM00207; TNF; 1.

FT NON_TER 1 169

FT SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;

Query Match 8.9%; Score 100; DB 11; Length 169;

Best Local Similarity 24.6%; Pred. No. 0.025;

Matches 32; Conservative 23; Mismatches 45; Indels 30; Gaps 5;

QY 71 LKRAPFKSWAYLQVAKHLNKTLSWKNK---GILHGVRYQDGNLVQFPGLYFIICQLQ 127

Db 40 LRRA-----AHLTGKPNRSRSPLEWEDTYGISLISGVKYQKGLVINDTGLYFYVSKYI 93

QY 128 FLVQ-CPNNSVDLKLLELLINKH-----IKKQALVTVCSGM-----QTKH 166

Db 94 FRGSCNNQLSHKVVKNKSKYPQDLVLMCKMKNYCTTGOMWARSSYLGAFFNFTSNDH 153

QY 167 VYQNLQFL 176

Db 154 LYVNVSELSL 163

RESULT 3

Q9BEE8 PRELIMINARY; PRT; 215 AA.

AC Q9BEE8;

DT 01-JUN-2001 (Tremblrel. 17, Created)

RT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DE TUMOR NECROSIS FACTOR PRECURSOR (FRAGMENT).

GN TNFA.

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.

OX NCBI_TaxID=9365;

RN [1]

RP SEQUENCE FROM N.A.

RA van Dijk M.A.M., de Jong W.W.;

RT "Indels indicate that rodents are monophyletic and lagomorphs are their sister group";

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases

DR EMBL; AJ286830; CAC28522.1; -

FT NON_TER 1 215

FT SEQUENCE 215 AA; 23696 MW; 3E337E7E65F074EA CRC64;

Query Match 8.6%; Score 96.5; DB 6; Length 133;

Best Local Similarity 23.3%; Pred. No. 0.075;

Matches 47; Conservative 36; Mismatches 76; Indels 43; Gaps 10;

QY 18 SYEYLTATIALCLVFTVATIMLVQRTDSIPNSPDNVPKGGNCSEDLILK--RAP 75

Db 28 SFFLVAGATTFLCLLH---FGVIGPQDE---FPDNIQLNNA-----LAVPLRSSRTQ 74

QY 76 FKKSWAYLQVAKHLNKTLSWKNKG---ILHGVRYQDGNLVQFPGLYFIICQLQFLVQ 131

Db 75 SDRPVAHV-VASIKSEQQLWSEVANALLANGKLTQNLVPLDGLYL---QVLFKQG 133

QY 132 -CPNNSVDLKLLELLINKHKK-----QALVTVCS-----GMQTHVYQNLQSF 174

Db 134 GCPSTHV-----FLTHNKRKYAVSYQKDVNLLSAIKSPCOSETPGEAE--HWVEPIYL 187

QY 175 LLDYLQVNTTISVNVDTFQYID 196

Db 188 GVQLEKGDRLSAEINLPDYID 209

RESULT 4

Q9BDN1 PRELIMINARY; PRT; 280 AA.

AC Q9BDN1;

DT 01-JUN-2001 (Tremblrel. 17, Created)

RT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DE CD95L PROTEIN.

GN CD95L.

OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Cercopithecidae; Cercopithecinae; Cercopithecus.

OX NCBI_TaxID=9531;

RN [1]

RP SEQUENCE FROM N.A.

RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,

RA Weiss W.R., Ansari A.A.;

RT "Cloning, sequencing and homology analysis of nonhuman Fas/Fas-Ligand and co-stimulatory molecules";

RL Immunogenetics 0:0-0(2001).

DR EMBL; AF344847; AAK37606.1; -

QY SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;

Query Match 8.5%; Score 95.5; DB 6; Length 280;

Best Local Similarity 27.1%; Pred. No. 0.13;

Matches 35; Conservative 21; Mismatches 46; Indels 27; Gaps 6;

QY 75 PFKKSW---AYLQVAKHLNKTLSWKNK-GI--LHGVRYQDGNLVQFPGLYFIICQLQ 128

Db 137 PEKKEQRKVAHLTKPNRSRSPLEWEDTYGIVLLSGVKYKKGGLVINEGTGLFYVSKYF 196

QY 129 LVQ-CPNNSVDLKLLELLINKH-----IKKQALVTVCSGM-----QTKHV 167

Db 197 RGQSCNTPLSHKVVKNKSKYPQDLVLMCKMKNYCTTGOMWARSSYLGAFFNLTSTDHL 256

QY 168 YQNLQFL 176

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 25, 2002, 08:35:55 ; Search time 19.25 seconds
(without alignments)
251.335 Million cell updates/sec

Title: US-09-628-126-23
Perfect score: 1118
Sequence: 1 MHPAGSVASHLGTTSRSYF.....DTSTFPLENVLSIFLYNSD 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Minimum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	215	1 US-08-225-989-23	Sequence 23, Appl
2	1118	100.0	215	1 US-08-570-923-23	Sequence 23, Appl
3	1118	100.0	215	1 US-08-580-014-23	Sequence 23, Appl
4	1118	100.0	215	4 US-09-079-785-23	Sequence 23, Appl
5	1118	100.0	234	1 US-08-225-989-8	Sequence 8, Appl1
6	1118	100.0	234	1 US-08-570-923-8	Sequence 8, Appl1
7	1118	100.0	234	1 US-08-580-014-8	Sequence 8, Appl1
8	1118	100.0	234	4 US-09-079-785-8	Sequence 8, Appl1
9	814.5	72.9	220	1 US-08-225-989-19	Sequence 19, Appl
10	814.5	72.9	220	1 US-08-570-923-19	Sequence 19, Appl
11	814.5	72.9	220	1 US-08-580-014-19	Sequence 19, Appl
12	814.5	72.9	220	4 US-09-079-785-19	Sequence 19, Appl
13	814.5	72.9	239	1 US-08-225-989-6	Sequence 6, Appl1
14	814.5	72.9	239	1 US-08-570-923-6	Sequence 6, Appl1
15	814.5	72.9	239	1 US-08-580-014-6	Sequence 6, Appl1
16	814.5	72.9	239	4 US-09-079-785-6	Sequence 6, Appl1
17	775	69.3	148	3 US-08-584-031-12	Sequence 12, Appl
18	592	53.0	125	1 US-08-225-989-20	Sequence 20, Appl
19	592	53.0	125	1 US-08-570-923-20	Sequence 20, Appl
20	592	53.0	125	1 US-08-580-014-20	Sequence 20, Appl
21	592	53.0	125	4 US-09-079-785-20	Sequence 20, Appl
22	447.5	40.0	130	1 US-08-225-989-21	Sequence 21, Appl
23	447.5	40.0	130	1 US-08-570-923-21	Sequence 21, Appl
24	447.5	40.0	130	1 US-08-580-014-21	Sequence 21, Appl
25	447.5	40.0	130	4 US-09-079-785-21	Sequence 21, Appl
26	274	24.5	52	4 US-09-369-494-17	Sequence 17, Appl
27	274	24.5	52	4 US-09-358-569D-15	Sequence 15, Appl

28 102 9.1 279 5 PCT-US95-00362-5
29 92 8.2 378 3 US-08-630-172-21
30 92 8.2 378 4 US-09-375-419-21
31 91.5 8.1 376 3 US-08-751-512-8
32 90.5 8.1 145 3 US-08-630-172-5
33 90.5 8.1 145 4 US-09-375-419-5
34 90.5 8.1 179 3 US-08-649-100-9
35 90.5 8.1 281 2 US-08-810-453-2
36 90.5 8.1 281 3 US-08-815-190A-2
37 90.5 8.1 281 4 US-09-290-640-25
38 90.5 8.1 281 4 US-09-479-524-3
39 90.5 8.1 281 5 PCT-US95-00362-2
40 90.5 8.1 287 3 US-08-815-190A-16
41 90 8.1 141 4 US-09-286-529-22
42 90 8.1 149 3 US-08-584-031-17
43 86 7.7 158 1 US-07-994-469A-99
44 85.5 7.6 309 1 US-08-236-918A-2
45 85 7.6 161 1 US-07-994-469A-61

ALIGNMENTS

RESULT 1
US-08-225-989-23
Sequence 23, Application US/08225989
Patent No. 548981
GENERAL INFORMATION:
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
APPLICANT: Armistage, Richard J.
APPLICANT: Gruss, Hans-Jurgen
TITLE OF INVENTION: No. 5480981el Cytokine That Binds 1030
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Seese, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,989
FILING DATE: 12 APRIL 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/966,775
FILING DATE: 27-OCT-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 907,224
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,660
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 892,459
FILING DATE: 02-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 889,717
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2804-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644

Sequence 5, Appli
Sequence 21, Appl
Sequence 21, Appl
Sequence 8, Appli
Sequence 5, Appli
Sequence 9, Appli
Sequence 2, Appli
Sequence 25, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 16, Appli
Sequence 22, Appli
Sequence 17, Appli
Sequence 99, Appli
Sequence 2, Appli
Sequence 61, Appli

TELEX: 756822

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-225-989-23

Query Match

Best Local Similarity 100.0%; Score 1118; DB 1; Length 215;

Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPLG 60

Db 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPLG 60

61 GNCSEDLILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYODGNLVIQFPGLY 120

Db 61 GNCSEDLILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYODGNLVIQFPGLY 120

QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMOTKHVYQNLQSFLLDYIQ 180

Db 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMOTKHVYQNLQSFLLDYIQ 180

QY 181 VNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 215

Db 181 VNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 215

RESULT 2

US-08-570-923-23

Sequence 23, Application US/08570923

Patent No. 5677430

GENERAL INFORMATION:

APPLICANT: Goodwin, Raymond G.

APPLICANT: Smith, Craig A.

APPLICANT: Armitage, Richard J.

APPLICANT: Gruss, Hans-Jurgen

TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kathryn A. Seese, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/570,923

FILING DATE: 12-DEC-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/225,989

FILING DATE: 12 APRIL 1994

APPLICATION NUMBER: US 07/966,775

FILING DATE: 27-OCT-1992

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 907,224

FILING DATE: 01-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 899,660

FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 892,459

FILING DATE: 02-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 889,717

FILING DATE: 26-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2804-E

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-570-923-23

Query Match

Best Local Similarity 100.0%; Score 1118; DB 1; Length 215;

Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPLG 60

Db 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPLG 60

QY 61 GNCSEDLILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYODGNLVIQFPGLY 120

Db 61 GNCSEDLILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVRYODGNLVIQFPGLY 120

QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMOTKHVYQNLQSFLLDYIQ 180

Db 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCESGMOTKHVYQNLQSFLLDYIQ 180

QY 181 VNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 215

Db 181 VNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 215

RESULT 3

US-08-580-014-230

Sequence 23, Application US/08580014

Patent No. 5753243

GENERAL INFORMATION:

APPLICANT: Goodwin, Raymond G.

APPLICANT: Smith, Craig A.

APPLICANT: Armitage, Richard J.

APPLICANT: Gruss, Hans-Jurgen

TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kathryn A. Seese, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/580,014

FILING DATE: 20-DEC-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/225,989

FILING DATE: 12 APRIL 1994

APPLICATION NUMBER: US 07/966,775

FILING DATE: 27-OCT-1992